During this teleconference, Mr. Tracy explained to Examiner Stole that the originally filed Sequence Listing contained three typographical errors (identified in detail below). Mr. Tracy discussed with Examiner Stole what evidence would be required to correct the typographical errors. Based on this discussion, and a follow-up discussion between Kevin Hooper of this firm and Examiner Stole on May 16, 2001, the applicants undertook costly and time-intensive lab work to demonstrate that the errors in the originally filed Sequence Listing are typographical in nature and that one skilled in the art would readily recognize these errors and how to remedy them by sequencing the clone identified in the present application, which is publically available. (*See In re Oda*, 170 USPQ 268 (CCPA 1971).

The substitute Sequence Listing corrects the following three typographical errors present in the original Sequence Listing:

(1) the nucleotide at position 852 of SEQ ID NO:1 has been changed from "G" to --C--;

(2) the nucleotide at position 644 of SEQ ID NO:3 has been changed from "A" to --C--; and

(3) the amino acid at position 192 of SEQ ID NO:7 has been changed from "Asn" to --Thr--.

The corrections contained in the substitute Sequence Listing are supported by the deposit of the strain from which SEQ ID NOs:1, 3 and 7 were obtained under the terms of the Budapest Treaty at the Deutsche Sammlung Von Mikroorganismen, Grisebachstrasse, D-3400 Gottingen, Germany, under Deposit No.: DSM 4025 on

March 17, 1987, and the reference to the deposit in the specification (*see* page 8, lines 9-11).

The evidence supporting the requested correction is submitted concurrently herewith in the form of declarations by the scientist who commissioned the sequencing on behalf of the applicants, and employees of independent cloning and sequencing companies who cloned and sequenced the relevant parts of the deposited clone. *See* Exhibits C-F. no such exhibits

Claims 4 and 5 have been amended to replace the term "DNA" with --isolated nucleic acid--. In view of the amendment to claim 4, claim 11, which depends form claim 4, has been amended to replace the term "DNA" with --nucleic acid--. Support for these amendments can be found in the specification at, for example, page 8, line 18 to page 9, line 3, and page 10, lines 11-16.

Claims 10 and 11 have been amended to replace the term "recombinant organism comprising" with --host cell transformed with--. Support for this amendment can be found in original claim 12 and in the specification at, for example, page 8, line 18 to page 9, line 3, and page 12, lines 13-19.

Claim 29 has been amended to specify that the recited "isolated polynucleotide" comprises SEQ ID NO:1. Support for this amendment can be found in the Sequence Listing submitted with the original application and in the specification at, for example, page 16, lines 1-7.

Claim 30 has been amended to specify that the recited "isolated polynucleotide" comprises "a polynucleotide sequence encoding a polypeptide fragment consisting of amino acid residues 1 to 95 of SEQ ID NO:5." Support for this amendment

can be found in Figure 4 and in the Sequence Listing, which were submitted with the original application, and in the specification at, for example, page 60, line 13.

Claim 31 has been amended to specify that the recited "isolated polynucleotide" comprises "a polynucleotide sequence encoding a polypeptide fragment consisting of amino acid residues 1 to 135 of SEQ ID NO:5." Support for this amendment can be found in Figure 4 and in the Sequence Listing, which were submitted with the original application, and in the specification at, for example, page 60, line 11.

It is submitted that no new matter has been introduced by the foregoing amendments. Approval and entry of the amendments is respectfully requested.

Substitute Sequence Listing

We thank the prior Examiner for the courtesies extended during the telephonic Interviews ("Interviews") conducted with Tim Tracy and Kevin Hooper of our offices on June 23, 1999 and May 16, 2001, respectively. In accordance with comments made by the Examiner during the Interviews, the Specification has been amended to replace the existing Sequence Listing with a substitute Sequence Listing that corrects three typographical errors, as set forth above. A paper copy of the Sequence Listing is attached hereto as Exhibit A and a computer readable form of the Sequence Listing is attached hereto as Exhibit G.

In accordance with 37 CFR § 1.825(b), upon information and belief, the content of the paper copy and the computer readable form of the Sequence Listing submitted herewith are, upon information and belief, identical.

In support of the corrections embodied in the substitute Sequence Listing and as recommended by the Examiner during the Interviews, we have attached as Exhibits C-F, respectively, the First Declaration of Dr. Masako Shinjoh under 37 C.F.R. §1.132 ("First Shinjoh Declaration"), the Second Declaration of Dr. Masako Shinjoh under 37 C.F.R. §1,132 ("Second Shinjoh Declaration"), the Declaration of Mr. Yoshitaka Murata under 37 C.F.R. §1.132 ("Murata Declaration"), and the Declaration of Mr. Masao Mashita under 37 C.F.R. §1.132 ("Mashita Declaration").

Dr. Shinjoh, a genetic engineer at Nippon Roche Research Center of Nippon Roche K.K. ("Roche") and a coinventor of the instant application (*see* First and Second Shinjoh Decls. ¶¶ 1 and 2), attests that after the instant application was filed she became aware of the following typographical errors in the originally filed Sequence Listing:

(1) the nucleotide at position 852 of SEQ ID NO:1 is a "G," but it should be a "C";

(2) the nucleotide at position 644 of SEQ ID NO:3 is an "A," but it should be a "C"; and

(3) the amino acid at position 192 of SEQ ID NO:7 is "Asn," but it should be "Thr".

(*See* Second Shinjoh Decl. ¶¶ 4-9). In accordance with Examiner Stole's guidance, to confirm these errors, Dr. Shinjoh commissioned the independent sequencing of strain DSM 4025, the same strain from which SEQ ID NOs: 1 and 3 were isolated, and from which SEQ ID NO: 7 was derived. (*See* page 17, lines 14-17 and Example 1 on pages

27-33). The deposit of strain DSM 4025 is specifically referenced in the specification. (*See* page 8, lines 9-11).

Dr. Shinjoh obtained a sample of strain DSM 4025 from the Deutsche Sammlung Von Mikroorganismen und Zellkulturen GmbH ("DSMZ") (*see* Second Shinjoh Decl. at ¶¶ 6-9). Dr. Shinjoh then forwarded the sample of DSM 4025 to Mr. Masao Mashita for sequencing at an independent cloning and sequencing company. (*See* First Shinjoh Decl. ¶¶ 10-12).

Mr. Mashita, Sales & Marketing Director at Sawady Technology Co., Ltd. (*see* Mashita Decl. ¶ 1), then forwarded the sample of DSM 4025 received from Dr. Shinjoh to Mr. Yoshitaka Murata at another company independent from Roche for the isolation of chromosomal DNA (*see Id.* ¶¶ 6 and 7). Mr. Murata, a scientist at K.K. Kyurin Corporation (*see* Murata Decl. ¶ 1), supervised the isolation of chromosomal DNA from the sample of DSM 4025 and forwarded the isolated DNA to Mr. Mashita (*see Id.* at ¶¶ 7-10). Mr. Mashita then supervised the sequencing of the DNA (*see* Mashita Decl. ¶¶ 8 and 9) and forwarded the resulting sequence to Dr. Shinjoh (*see Id.* at ¶ 10).

Upon receipt of the nucleotide sequence obtained from DSM 4025, Dr. Shinjoh was able to confirm that in fact, the Sequence Listing originally filed with the instant application contained the aforementioned three errors. (Second Shinjoh Decl. ¶¶ 16-20).

As the Federal Circuit has recently confirmed, reference in a patent specification to a deposit of genetic material is sufficient to fully describe that material. *See Enzo Biochem Inc. v. Gen-Probe Inc.*, 63 USPQ2d 1609, 1614 (Fed. Cir. 2002) ("[R]eference in the specification to deposits of nucleotide sequences describe those

sequences sufficiently to the public for purposes of meeting the written description requirement."). In view of the reference to the deposit of strain DSM 4025 in the specification (*see* page 8, lines 9-11), the Declarations submitted herewith and the discussions with the Examiner during the Interviews, the identified errors would have been obvious to one skilled in the art as well their remedy. Thus, the proposed corrections are not new matter. (*In re Oda*, 170 USPQ at 271). Accordingly, entry and approval of the substitute Sequence Listing correcting the aforementioned errors is respectfully requested.

Objections

The Examiner objected to claim 16 "as being dependent upon a rejected base claim 10." (Paper No. 16 at 9). However, we note that claim 16 is an independent claim and is ***not*** dependent on claim 10. Accordingly, it is respectfully submitted that this objection is moot and should be withdrawn.

§101 Rejections

Claims 4 and 5 were rejected under 35 U.S.C. § 101. In making the rejection, the Examiner asserted that "[i]n the absence of the hand of man, naturally occurring proteins and/or nucleic acids are considered non-statutory subject matter." (Paper No. 16 at 2). The Examiner suggested that "[t]his rejection may be overcome by amending the claims to contain wording such as 'An isolated nucleic acid'." (*Id.* at 2-3).

With a view towards furthering prosecution and in accordance with the Examiner's recommendation, claims 4 and 5 have been amended to recite "an isolated

nucleic acid." Accordingly, it is respectfully submitted that the rejection is rendered moot and should be withdrawn.

Claims 10 and 11 also were rejected under 35 U.S.C. § 101. In making the rejection, the Examiner asserted that "the claimed invention is directed toward non-statutory subject matter. These claims include humans within their scope." (Paper No. 16 at 3). The Examiner suggested that "[t]his rejection may be overcome by amending the claims to contain wording such as 'A host cell transformed…'." (*Id.*).

With a view towards furthering prosecution and in accordance with the Examiner's recommendation, claims 10 and 11 have been amended to recite "a host cell transformed...." Accordingly, it is respectfully submitted that the rejection is rendered moot and should be withdrawn.

§112 Second Paragraph Rejections

Claim 30 was rejected under 35 U.S.C. 112, second paragraph. In making the rejection, the Examiner asserted that claim 30 "is confusing as to whether the fragment of SEQ ID NO:5 has AADH activity." (Paper No. 16 at 4).

With a view towards furthering prosecution, claim 30 has been amended to remove the recitation of "alcohol and aldehyde dehydrogenase activity" (*i.e.*, AADH acitivity) and to recite a specific fragment "consisting of amino acid residues 1 to 95 of SEQ ID NO:5" as suggested by the Examiner. Accordingly, it is respectfully submitted that the rejection is rendered moot and should be withdrawn.

Claim 35 was rejected as being identical to originally filed claim 12. (*See* Paper No. 16 at 5). With a view towards furthering prosecution, claim 35 has been

cancelled, without prejudice. Accordingly, it is respectfully submitted that the rejection is rendered moot and should be withdrawn.

§112 First Paragraph Rejections

1. Written Description

Claims 8 and 33 were rejected under 35 U.S.C. 112, first paragraph, "because the specification does not disclose a repeatable process to obtain the vector pSSA102R." (Paper No. 16 at 5). In making the rejection, the Examiner asserted that "a deposit of this vector [pSSA102R] should have been made." (*Id.*).

In response, the following statements are provided upon information and belief:

The pSSA102R vector was deposited under the terms of the Budapest Treaty at the Deutsche Sammlung Von Mikroorganismen und Zellkulturen GmbH ("DSMZ"), Mascheroder Weg 1b, D-38124 Braunschweig, Germany, under Deposit No.: DSM 14798 on February 1, 2002. Confirmation of this deposit is attached hereto as Exhibit H.

All restrictions imposed by the depositor on the availability to the public of the deposited material mentioned will be irrevocably removed upon the granting of a patent.

In view of the statements set forth above, it is respectfully submitted that the rejection of claims 8 and 33 is rendered moot and should be withdrawn.

Claim 29 was rejected under 35 USC §112, first paragraph. (Paper No. 16 at 5-6). In making the rejection, the Examiner asserted that "the disclosure does not

set forth DNA molecules encoding polypeptides having sequences that are at least 80% identical to SEQ ID NO:5," and that "[n]either the claim nor the specification contain any disclosure of the function of ***all*** the polypeptide sequences that are at least 80% identical to SEQ ID NO:5." (emphasis added) (*Id.*).

Initially we note that, as is well settled, the written description requirement for a claimed genus may be satisfied by sufficient description of a ***representative number of species***. *See Regents of University of California v. Eli Lilly & Co.*, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997); and MPEP § 2163 (II)(A)(3)(a)(ii). It is submitted that nowhere in the MPEP nor in existing legal precedent is there to be found the requirement that ***all*** of the polypeptide sequences in a genus of polypeptides sequences must be described. For this reason alone, the rejection should be withdrawn.

Notwithstanding the legal deficiencies of the rejection, and with a view towards furthering prosecution, claim 29 has been amended to remove the recitation of sequences that are 80% identical to SEQ ID NO: 5. Accordingly, it is respectfully submitted that the rejection is rendered moot and should be withdrawn.

Claim 31 also was rejected under 35 USC §112, first paragraph. (Paper No. 16 at 6-7). In making the rejection, the Examiner asserted that "the disclosure does not set forth DNA molecules encoding polypeptides having sequences that are at least 80% identical to SEQ ID NO:5." (*Id.* at 6).

With a view towards furthering prosecution, claim 31 has been amended to remove the recitation of sequences that are 80% identical to SEQ ID NO: 5. Accordingly, it is respectfully submitted that the rejection is rendered moot and should be withdrawn.

2. Enablement

Claims 10 and 11 were rejected under 35 U.S.C. § 112, first paragraph. (Paper No. 16 at 5). In making the rejection, the Examiner asserted that "the specification... does not reasonably provide enablement for all possible host organisms ... transformed or transfected" with the claimed plasmids. (*Id.*). However, the Examiner acknowledged that the specification is "enabling for ***host cells*** transformed or transfected with the claimed plasmids." (emphasis added) (*Id.*).

With a view towards furthering prosecution, claims 10 and 11 have been amended as suggested by the Examiner to recite "a host cell transformed...." Accordingly, it is respectfully submitted that the rejection is rendered moot and should be withdrawn.

Claims 29 and 31 were rejected under 35 U.S.C. § 112, first paragraph. (Paper No. 16 at 7). In making the rejection, the Examiner acknowledged that the specification was "enabling for the DNA molecule of SEQ ID NO:1, or DNA encoding SEQ ID NO:5, that contain a 45 amino acid fragment having alcohol and aldehyde dehydrogenase activity." (*Id.*). The Examiner asserted, however, that the specification "does not reasonably provide enablement for DNA encoding polypeptides having at least 80% identity to SEQ ID NO:5 or polynucleotides which encode a fragment of at least 45 amino acid residues of polypeptides having at least 80% identity to SEQ ID NO:5." (*Id.*).

With a view towards furthering prosecution, claims 29 and 31 have been amended to remove the recitation of sequences that are 80% identical to SEQ ID NO: 5.

Accordingly, it is respectfully submitted that the rejection is rendered moot and should be withdrawn.

In view of the foregoing, entry of and approval of the amendments, and allowance of all the claims, respectfully, is requested. If the Examiner has any questions regarding this paper, please contact the undersigned attorney.

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to Commissioner for Patents, Washington, D.C. 20231, on December 4, 2002.

Gonzalo Merino

Respectfully submitted,

By: _____

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E-A

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Ojima, Setsuko
Shinjoh, Masako
Tomiyama, Noribumi

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gaaaatatgg gccgcatcga cgcgattgat atcagcaccg ggcgcacctt gtggtcggcg 1440

gagcgccctg cggcgaacta ctcgcccgtt ttgtcgacgg caggcggtgt ggtgttcaac 1500

ggcgggaccg accgctattt ccgtgccctc agccaggaaa ccggcgagac tttgtggcag 1560

B1 Cont.

gcccgtcttg cgacggtcgc gacggggcag gcgatcagct acgagttgga cggcgtgcaa 1620

tatatcgcca tcggtgcggg cggtctgacc tatggcacgc aattgaacgc gccgctggcc 1680

gaggcaatcg attcgacctc ggtcggtaat gcgatctatg tctttgcact gccgcagtaa 1740

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<211> 579
<212> PRT
<213> Gluconobacter oxydans

<220>
<221> SIGNAL
<222> (1)..(23)
<223>

<400> 5

Met Lys Pro Thr Ser Leu Leu Trp Ala Ser Ala Gly Ala Leu Ala Leu
1 5 10 15

Leu Ala Ala Pro Ala Phe Ala Gln Val Thr Pro Val Thr Asp Glu Leu
20 25 30

Leu Ala Asn Pro Pro Ala Gly Glu Trp Ile Ser Tyr Gly Gln Asn Gln
35 40 45

Glu Asn Tyr Arg His Ser Pro Leu Thr Gln Ile Thr Thr Glu Asn Val
50 55 60

Gly Gln Leu Gln Leu Val Trp Ala Arg Gly Met Gln Pro Gly Lys Val
65 70 75 80

Gln Val Thr Pro Leu Ile His Asp Gly Val Met Tyr Leu Ala Asn Pro
85 90 95

Gly Asp Val Ile Gln Ala Ile Asp Ala Lys Thr Gly Asp Leu Ile Trp
100 105 110

Glu His Arg Arg Gln Leu Pro Asn Ile Ala Thr Leu Asn Ser Phe Gly
115 120 125

Glu Pro Thr Arg Gly Met Ala Leu Tyr Gly Thr Asn Val Tyr Phe Val
130 135 140

B1 Cont

Ser Trp Asp Asn His Leu Val Ala Leu Asp Thr Ala Thr Gly Gln Val
145 150 155 160

Thr Phe Asp Val Asp Arg Gly Gln Gly Glu Asp Met Val Ser Asn Ser
165 170 175

Ser Gly Pro Ile Val Ala Asn Gly Val Ile Val Ala Gly Ser Thr Cys
180 185 190

Gln Tyr Ser Pro Phe Gly Cys Phe Val Ser Gly His Asp Ser Ala Thr
195 200 205

Gly Glu Glu Leu Trp Arg Asn Tyr Phe Ile Pro Arg Ala Gly Glu Glu
210 215 220

Gly Asp Glu Thr Trp Gly Asn Asp Tyr Glu Ala Arg Trp Met Thr Gly
225 230 235 240

Ala Trp Gly Gln Ile Thr Tyr Asp Pro Val Thr Asn Leu Val His Tyr
245 250 255

Gly Ser Thr Ala Val Gly Pro Ala Ser Glu Thr Gln Arg Gly Thr Pro
260 265 270

Gly Gly Thr Leu Tyr Gly Thr Asn Thr Arg Phe Ala Val Arg Pro Asp
275 280 285

Thr Gly Glu Ile Val Trp Arg His Gln Thr Leu Pro Arg Asp Asn Trp
290 295 300

B1 Cont

Asp Gln Glu Cys Thr Phe Glu Met Met Val Thr Asn Val Asp Val Gln
305 310 315 320

Pro Ser Thr Glu Met Glu Gly Leu Gln Ser Ile Asn Pro Asn Ala Ala
325 330 335

Thr Gly Glu Arg Arg Val Leu Thr Gly Val Pro Cys Lys Thr Gly Thr
340 345 350

Met Trp Gln Phe Asp Ala Glu Thr Gly Glu Phe Leu Trp Ala Arg Asp
355 360 365

Thr Asn Tyr Gln Asn Met Ile Glu Ser Ile Asp Glu Asn Gly Ile Val
370 375 380

Thr Val Asn Glu Asp Ala Ile Leu Lys Glu Leu Asp Val Glu Tyr Asp
385 390 395 400

Val Cys Pro Thr Phe Leu Gly Gly Arg Asp Trp Pro Ser Ala Ala Leu
405 410 415

Asn Pro Asp Ser Gly Ile Tyr Phe Ile Pro Leu Asn Asn Val Cys Tyr
420 425 430

Asp Met Met Ala Val Asp Gln Glu Phe Thr Ser Met Asp Val Tyr Asn
435 440 445

Thr Ser Asn Val Thr Lys Leu Pro Pro Gly Lys Asp Met Ile Gly Arg
450 455 460

Ile Asp Ala Ile Asp Ile Ser Thr Gly Arg Thr Leu Trp Ser Val Glu
465 470 475 480

Arg Ala Ala Ala Asn Tyr Ser Pro Val Leu Ser Thr Gly Gly Gly Val
485 490 495

Leu Phe Asn Gly Gly Thr Asp Arg Tyr Phe Arg Ala Leu Ser Gln Glu
500 505 510

Thr Gly Glu Thr Leu Trp Gln Thr Arg Leu Ala Thr Val Ala Ser Gly
515 520 525

Gln Ala Ile Ser Tyr Glu Val Asp Gly Met Gln Tyr Val Ala Ile Ala
530 535 540

Gly Gly Gly Val Ser Tyr Gly Ser Gly Leu Asn Ser Ala Leu Ala Gly
545 550 555 560

Glu Arg Val Asp Ser Thr Ala Ile Gly Asn Ala Val Tyr Val Phe Ala
565 570 575

Leu Pro Gln

B1 Cont.

<210> 6
<211> 579
<212> PRT
<213> Gluconobacter oxydans

<220>
<221> SIGNAL
<222> (1)..(23)
<223>

<400> 6

Met Lys Thr Ser Ser Leu Leu Val Ala Ser Val Ala Ala Leu Ala Ser
1 5 10 15

Tyr Ser Ser Phe Ala Leu Ala Gln Val Thr Pro Val Thr Asp Glu Leu
20 25 30

Leu Ala Asn Pro Pro Ala Gly Glu Trp Ile Ser Tyr Gly Gln Asn Gln
35 40 45

Glu Asn Tyr Arg His Ser Pro Leu Thr Gln Ile Thr Thr Glu Asn Val
50 55 60

Gly Gln Leu Gln Leu Val Trp Ala Arg Gly Met Gln Pro Gly Lys Val
65 70 75 80

Gln Val Thr Pro Leu Ile His Asp Gly Val Met Tyr Leu Ala Asn Pro
85 90 95

Gly Asp Val Ile Gln Ala Ile Asp Ala Lys Thr Gly Asp Leu Ile Trp
100 105 110

Glu His Arg Arg Gln Leu Pro Asn Ile Ala Thr Leu Asn Ser Phe Gly
115 120 125

Glu Pro Thr Arg Gly Met Ala Leu Tyr Gly Thr Asn Val Tyr Phe Val
130 135 140

Ser Trp Asp Asn His Leu Val Ala Leu Asp Thr Ala Thr Gly Gln Val
145 150 155 160

Thr Phe Asp Val Asp Arg Gly Gln Gly Glu Asp Met Val Ser Asn Ser

B1 Cont.

165 170 175

Ser Gly Pro Ile Val Ala Asn Gly Val Ile Val Ala Gly Ser Thr Cys
180 185 190

Gln Tyr Ser Pro Phe Gly Cys Phe Val Ser Gly His Asp Ser Ala Thr
195 200 205

Gly Glu Glu Leu Trp Arg Asn Tyr Phe Ile Pro Arg Ala Gly Glu Glu
210 215 220

Gly Asp Glu Thr Trp Gly Asn Asp Tyr Glu Ala Arg Trp Met Thr Gly
225 230 235 240

Val Trp Gly Gln Ile Thr Tyr Asp Pro Val Gly Gly Leu Val His Tyr
245 250 255

Gly Ser Ser Ala Val Gly Pro Ala Ser Glu Thr Gln Arg Gly Thr Thr
260 265 270

Gly Gly Thr Met Tyr Gly Thr Asn Thr Arg Phe Ala Val Arg Pro Glu
275 280 285

Thr Gly Glu Ile Val Trp Arg His Gln Thr Leu Pro Arg Asp Asn Trp
290 295 300

Asp Gln Glu Cys Thr Phe Glu Met Met Val Ala Asn Val Asp Val Gln
305 310 315 320

Pro Ala Ala Asp Met Asp Gly Val Arg Ser Ile Asn Pro Asn Ala Ala
325 330 335

Thr Gly Glu Arg Arg Val Leu Thr Gly Val Pro Cys Lys Thr Gly Thr
340 345 350

Met Trp Gln Phe Asp Ala Glu Thr Gly Glu Phe Leu Trp Ala Arg Asp
355 360 365

Thr Ser Tyr Glu Asn Ile Ile Glu Ser Ile Asp Glu Asn Gly Ile Val
370 375 380

31 Cont.

Thr Val Asp Glu Ser Lys Val Leu Thr Glu Leu Asp Thr Pro Tyr Asp
385 390 395 400

Val Cys Pro Leu Leu Leu Gly Gly Arg Asp Trp Pro Ser Ala Ala Leu
405 410 415

Asn Pro Asp Thr Gly Ile Tyr Phe Ile Pro Leu Asn Asn Thr Cys Met
420 425 430

Asp Ile Glu Ala Val Asp Gln Glu Phe Ser Ser Leu Asp Val Tyr Asn
435 440 445

Gln Ser Leu Thr Ala Lys Met Ala Pro Gly Lys Glu Leu Val Gly Arg
450 455 460

Ile Asp Ala Ile Asp Ile Ser Thr Gly Arg Thr Leu Trp Thr Ala Glu
465 470 475 480

Arg Glu Ala Ser Asn Tyr Ala Pro Val Leu Ser Thr Ala Gly Gly Val
485 490 495

Leu Phe Asn Gly Gly Thr Asp Arg Tyr Phe Arg Ala Leu Ser Gln Glu
500 505 510

Thr Gly Glu Thr Leu Trp Gln Thr Arg Leu Ala Thr Val Ala Ser Gly
515 520 525

Gln Ala Val Ser Tyr Glu Ile Asp Gly Val Gln Tyr Ile Ala Ile Gly
530 535 540

B1 Cont

Gly Gly Gly Thr Thr Tyr Gly Ser Phe His Asn Arg Pro Leu Ala Glu
545 550 555 560

Pro Val Asp Ser Thr Ala Ile Gly Asn Ala Met Tyr Val Phe Ala Leu
565 570 575

Pro Gln Gln

<210> 7
<211> 578
<212> PRT

<213> Gluconobacter oxydans

<220>
<221> SIGNAL
<222> (1)..(23)
<223>

<400> 7

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Met Lys Leu Thr Thr Leu Leu Gln Ser Ser Ala Ala Leu Leu Val Leu
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Gly Thr Ile Pro Ala Leu Ala Gln Thr Ala Ile Thr Asp Glu Met Leu
            20                  25                  30

Ala Asn Pro Pro Ala Gly Glu Trp Ile Asn Tyr Gly Gln Asn Gln Glu
        35                  40                  45

Asn Tyr Arg His Ser Pro Leu Thr Gln Ile Thr Ala Asp Asn Val Gly
    50                  55                  60

Gln Leu Gln Leu Val Trp Ala Arg Gly Met Glu Ala Gly Lys Ile Gln
65                  70                  75                  80

Val Thr Pro Leu Val His Asp Gly Val Met Tyr Leu Ala Asn Pro Gly
                85                  90                  95

Asp Val Ile Gln Ala Ile Asp Ala Ala Thr Gly Asp Leu Ile Trp Glu
            100                 105                 110

His Arg Arg Gln Leu Pro Asn Ile Ala Thr Leu Asn Ser Phe Gly Glu
        115                 120                 125

Pro Thr Arg Gly Met Ala Leu Tyr Gly Thr Asn Val Tyr Phe Val Ser
    130                 135                 140

Trp Asp Asn His Leu Val Ala Leu Asp Thr Ser Thr Gly Gln Val Val
145                 150                 155                 160

Phe Asp Val Asp Arg Gly Gln Gly Thr Asp Met Val Ser Asn Ser Ser
                165                 170                 175

Gly Pro Ile Val Ala Asn Gly Val Ile Val Ala Gly Ser Thr Cys Gln
            180                 185                 190
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B1 Cont.

Tyr Ser Pro Phe Gly Cys Phe Val Ser Gly His Asp Ser Ala Thr Gly
195 200 205

Glu Glu Leu Trp Arg Asn Thr Phe Ile Pro Arg Ala Gly Glu Glu Gly
210 215 220

Asp Glu Thr Trp Gly Asn Asp Tyr Glu Ala Arg Trp Met Thr Gly Val
225 230 235 240

Trp Gly Gln Ile Thr Tyr Asp Pro Val Gly Gly Leu Val His Tyr Gly
245 250 255

Thr Ser Ala Val Gly Pro Ala Ala Glu Ile Gln Arg Gly Thr Val Gly
260 265 270

Gly Ser Met Tyr Gly Thr Asn Thr Arg Phe Ala Val Arg Pro Glu Thr
275 280 285

Gly Glu Ile Val Trp Arg His Gln Thr Leu Pro Arg Asp Asn Trp Asp
290 295 300

Gln Glu Cys Thr Phe Glu Met Met Val Val Asn Val Asp Val Gln Pro
305 310 315 320

Ser Ala Glu Met Glu Gly Leu His Ala Ile Asn Pro Asp Ala Ala Thr
325 330 335

Gly Glu Arg Arg Val Val Thr Gly Val Pro Cys Lys Asn Gly Thr Met
340 345 350

B1 Cont.

Trp Gln Phe Asp Ala Glu Thr Gly Glu Phe Leu Trp Ala Arg Asp Thr
355 360 365

Ser Tyr Gln Asn Leu Ile Glu Ser Val Asp Pro Asp Gly Leu Val His
370 375 380

Val Asn Glu Asp Leu Val Val Thr Glu Leu Glu Val Ala Tyr Glu Ile
385 390 395 400

Cys Pro Thr Phe Leu Gly Gly Arg Asp Trp Pro Ser Ala Ala Leu Asn

405 410 415

Pro Asp Thr Gly Ile Tyr Phe Ile Pro Leu Asn Asn Ala Cys Ser Gly
420 425 430

Met Thr Ala Val Asp Gln Glu Phe Ser Ser Leu Asp Val Tyr Asn Val
435 440 445

Ser Leu Asp Tyr Lys Leu Ser Pro Gly Ser Glu Asn Met Gly Arg Ile
450 455 460

Asp Ala Ile Asp Ile Ser Thr Gly Arg Thr Leu Trp Ser Ala Glu Arg
465 470 475 480

Tyr Ala Ser Asn Tyr Ala Pro Val Leu Ser Thr Gly Gly Gly Val Leu
485 490 495

Phe Asn Gly Gly Thr Asp Arg Tyr Phe Arg Ala Leu Ser Gln Glu Thr
500 505 510

Gly Glu Thr Leu Trp Gln Thr Arg Leu Ala Thr Val Ala Ser Gly Gln
515 520 525

Ala Ile Ser Tyr Glu Ile Asp Gly Val Gln Tyr Val Ala Ile Gly Arg
530 535 540

Gly Gly Thr Ser Tyr Gly Ser Asn His Asn Arg Ala Leu Thr Glu Arg
545 550 555 560

B1 Cont.

Ile Asp Ser Thr Ala Ile Gly Ser Ala Ile Tyr Val Phe Ala Leu Pro
565 570 575

Gln Gln

<210> 8
<211> 579
<212> PRT
<213> Gluconobacter oxydans

<220>
<221> SIGNAL
<222> (1)..(23)

<223>

<400> 8

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Met Asn Pro Thr Thr Leu Leu Arg Thr Ser Ala Ala Val Leu Leu Leu
1               5                  10                  15

Thr Ala Pro Ala Ala Phe Ala Gln Val Thr Pro Ile Thr Asp Glu Leu
            20                  25                  30

Leu Ala Asn Pro Pro Ala Gly Glu Trp Ile Asn Tyr Gly Arg Asn Gln
        35                  40                  45

Glu Asn Tyr Arg His Ser Pro Leu Thr Gln Ile Thr Ala Asp Asn Val
    50                  55                  60

Gly Gln Leu Gln Leu Val Trp Ala Arg Gly Met Glu Ala Gly Ala Val
65                  70                  75                  80

Gln Val Thr Pro Met Ile His Asp Gly Val Met Tyr Leu Ala Asn Pro
                85                  90                  95

Gly Asp Val Ile Gln Ala Leu Asp Ala Gln Thr Gly Asp Leu Ile Trp
            100                 105                 110

Glu His Arg Arg Gln Leu Pro Ala Val Ala Thr Leu Asn Ala Gln Gly
        115                 120                 125

Asp Arg Lys Arg Gly Val Ala Leu Tyr Gly Thr Ser Leu Tyr Phe Ser
    130                 135                 140

Ser Trp Asp Asn His Leu Ile Ala Leu Asp Met Glu Thr Gly Gln Val
145                 150                 155                 160

Val Phe Asp Val Glu Arg Gly Ser Gly Glu Asp Gly Leu Thr Ser Asn
                165                 170                 175

Thr Thr Gly Pro Ile Val Ala Asn Gly Val Ile Val Ala Gly Ser Thr
            180                 185                 190

Cys Gln Tyr Ser Pro Tyr Gly Cys Phe Ile Ser Gly His Asp Ser Ala
        195                 200                 205
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B1 Cont.

Thr Gly Glu Glu Leu Trp Arg Asn His Phe Ile Pro Gln Pro Gly Glu
210 215 220

Glu Gly Asp Glu Thr Trp Gly Asn Asp Phe Glu Ala Arg Trp Met Thr
225 230 235 240

Gly Val Trp Gly Gln Ile Thr Tyr Asp Pro Val Thr Asn Leu Val Phe
245 250 255

Tyr Gly Ser Thr Gly Val Gly Pro Ala Ser Glu Thr Gln Arg Gly Thr
260 265 270

Pro Gly Gly Thr Leu Tyr Gly Thr Asn Thr Arg Phe Ala Val Arg Pro
275 280 285

Asp Thr Gly Glu Ile Val Trp Arg His Gln Thr Leu Pro Arg Asp Asn
290 295 300

Trp Asp Gln Glu Cys Thr Phe Glu Met Met Val Ala Asn Val Asp Val
305 310 315 320

Gln Pro Ser Ala Glu Met Glu Gly Leu Arg Ala Ile Asn Pro Asn Ala
325 330 335

Ala Thr Gly Glu Arg Arg Val Leu Thr Gly Ala Pro Cys Lys Thr Gly
340 345 350

Thr Met Trp Ser Phe Asp Ala Ala Ser Gly Glu Phe Leu Trp Ala Arg
355 360 365

B1 Cont

Asp Thr Asn Tyr Thr Asn Met Ile Ala Ser Ile Asp Glu Thr Gly Leu
370 375 380

Val Thr Val Asn Glu Asp Ala Val Leu Lys Glu Leu Asp Val Glu Tyr
385 390 395 400

Asp Val Cys Pro Thr Phe Leu Gly Gly Arg Asp Trp Ser Ser Ala Ala
405 410 415

Leu Asn Pro Asp Thr Gly Ile Tyr Phe Leu Pro Leu Asn Asn Ala Cys
420 425 430

Tyr Asp Ile Met Ala Val Asp Gln Glu Phe Ser Ala Leu Asp Val Tyr
435 440 445

Asn Thr Ser Ala Thr Ala Lys Leu Ala Pro Gly Phe Glu Asn Met Gly
450 455 460

Arg Ile Asp Ala Ile Asp Ile Ser Thr Gly Arg Thr Leu Trp Ser Ala
465 470 475 480

Glu Arg Pro Ala Ala Asn Tyr Ser Pro Val Leu Ser Thr Ala Gly Gly
485 490 495

Val Val Phe Asn Gly Gly Thr Asp Arg Tyr Phe Arg Ala Leu Ser Gln
500 505 510

Glu Thr Gly Glu Thr Leu Trp Gln Ala Arg Leu Ala Thr Val Ala Thr
515 520 525

Gly Gln Ala Ile Ser Tyr Glu Leu Asp Gly Val Gln Tyr Ile Ala Ile
530 535 540

Gly Ala Gly Gly Leu Thr Tyr Gly Thr Gln Leu Asn Ala Pro Leu Ala
545 550 555 560

Glu Ala Ile Asp Ser Thr Ser Val Gly Asn Ala Ile Tyr Val Phe Ala
565 570 575

Leu Pro Gln

B1 Cont

<210> 9
<211> 82
<212> DNA
<213> synthetic oligonucleotide

<400> 9
catgaaaata aaaacaggtg cacgcatcct cgcattatcc gcattaacga cgatgatgtt 60

ttccgcctcg gctctcgccc ag 82

<210> 10
<211> 83

<212> DNA
<213> synthetic oligonucleotide

<400> 10
gttacctggg cgagagccga ggcggaaaac atcatcgtcg ttaatgcgga taatgcgagg 60

atgcgtgcac ctgtttttat ttt 83

<210> 11
<211> 27
<212> PRT
<213> Escherichia coli

<220>
<221> SIGNAL
<222> (1)..(26)
<223>

<400> 11

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
1 5 10 15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Gln
20 25

B1 cont

<210> 12
<211> 27
<212> DNA
<213> synthetic oligonucleotide

<400> 12
gttagcgcgg tggatcccca ttggagg 27

Exhibit B

"Marked Up" Amendments to Claims Pursuant to Rule 1.121(c)(1)(ii)

4. (Amended) An isolated nucleic acid [A DNA] molecule encoding a recombinant polypeptide comprising SEQ ID NO:5 or a polypeptide with at least 80% identity to SEQ ID NO:5, and having alcohol and aldehyde dehydrogenase (AADH) activity.

5. (Amended) An isolated nucleic acid [A DNA] molecule of claim 4, wherein the nucleic acid [DNA] molecule is selected from the group consisting of a linear DNA, a circular DNA and an insertion DNA fragment on a chromosome.

10. (Twice Amended) A host cell transformed with [recombinant organism comprising] the recombinant expression vector of claim 6.

11. (Twice Amended) A host cell transformed with [recombinant organism comprising] the nucleic acid [DNA] molecule of claim 4.

29. (Amended) An isolated polynucleotide comprising [selected from the group consisting of] SEQ ID NO:1 [, and polynucleotide sequences which encode a polypeptide with at least 80% identity to SEQ ID NO:5].

30. (Amended) An isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide [which encodes a] fragment [comprising at least 95 amino acid residues of a polypeptide with the sequence] consisting of amino acid residues 1 to 95 of SEQ ID NO:5 [, which fragment has an alcohol and aldehyde dehydrogenase activity].

31. (Amended) An isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide [which encodes a] fragment [comprising at least 44 amino acid residues of a polypeptide, the polypeptide having at least 80% identity to] consisting of amino acid residues 1 to 135 of SEQ ID NO:5 [and alcohol and aldehyde dehydrogenase activity].